

RAW SEQUENCE LISTING

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Application Serial Number: 09/744,679 A
Source: JFW16
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IFW16

RAW SEQUENCE LISTING

DATE: 09/21/2005

PATENT APPLICATION: US/09/744,679A

TIME: 11:25:15

Input Set : A:\108366.ST25.txt

Output Set: N:\CRF4\09212005\I744679A.raw

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3 <110> APPLICANT: BAR-SHAVIT, Rachel
5 <120> TITLE OF INVENTION: METHOD FOR TREATMENT OF INVASIVE CELLS
7 <130> FILE REFERENCE: 108366
9 <140> CURRENT APPLICATION NUMBER: US 09/744,679A
10 <141> CURRENT FILING DATE: 2001-04-11
12 <150> PRIOR APPLICATION NUMBER: PCT/IL99/00079
13 <151> PRIOR FILING DATE: 1999-02-05
15 <150> PRIOR APPLICATION NUMBER: IL 125698
16 <151> PRIOR FILING DATE: 1998-08-07
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn version 3.3
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23 <211> LENGTH: 25
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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34          20          25
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40 <213> ORGANISM: Homo sapiens
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53 <211> LENGTH: 24
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
57 <400> SEQUENCE: 3
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60 1          5          10          15
63 Glu Phe Pro Phe Ser Ala Leu Glu
64          20
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68 <211> LENGTH: 25
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 4

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75 1 5 10 15
78 Asp Thr His Glu Leu Pro Asp Ser Ser
79 20 25
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83 <211> LENGTH: 3480
84 <212> TYPE: DNA
85 <213> ORGANISM: Homo sapiens
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (225)..(1502)
92 <400> SEQUENCE: 5
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95 gctcgccgag ggtcgcttgg accctgatct taccgctggg caccctgcgc tctgcctgcc 120
97 gcgaagaccg gctccccgac ccgcagaagt caggagagag ggtgaagcgg agcagcccga 180
99 ggcggggcag cctcccgagg cagcgccgcg cagagcccgg gaca atg ggg ccg cgg 236
100 Met Gly Pro Arg
101 1
103 cgg ctg ctg ctg gtg gcc gcc tgc ttc agt ctg tgc ggc ccg ctg ttg 284
104 Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys Gly Pro Leu Leu
105 5 10 15 20
107 tct gcc cgc acc cgg gcc cgc agg cca gaa tca aaa gca aca aat gcc 332
108 Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys Ala Thr Asn Ala
109 25 30 35
111 acc tta gat ccc cgg tca ttt ctt ctc agg aac ccc aat gat aaa tat 380
112 Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr
113 40 45 50
115 gaa cca ttt tgg gag gat gag gag aaa aat gaa agt ggg tta act gaa 428
116 Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser Gly Leu Thr Glu
117 55 60 65
119 tac aga tta gtc tcc atc aat aaa agc agt cct ctt caa aaa caa ctt 476
120 Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu Gln Lys Gln Leu
121 70 75 80
123 cct gca ttc atc tca gaa gat gcc tcc gga tat ttg acc agc tcc tgg 524
124 Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu Thr Ser Ser Trp
125 85 90 95 100
127 ctg aca ctc ttt gtc cca tct gtg tac acc gga gtg ttt gta gtc agc 572
128 Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val Phe Val Val Ser
129 105 110 115
131 ctc cca cta aac atc atg gcc atc gtt gtg ttc atc ctg aaa atg aag 620
132 Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile Leu Lys Met Lys
133 120 125 130
135 gtc aag aag ccg gcg gtg gtg tac atg ctg cac ctg gcc acg gca gat 668
136 Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu Ala Thr Ala Asp
137 135 140 145
139 gtg ctg ttt gtg tct gtg ctc ccc ttt aag atc agc tat tac ttt tcc 716
140 Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser Tyr Tyr Phe Ser
141 150 155 160
143 ggc agt gat tgg cag ttt ggg tct gaa ttg tgt cgc ttc gtc act gca 764

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144	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg	Phe	Val	Thr	Ala	
145	165					170					175					180	
147	gca	ttt	tac	tgt	aac	atg	tac	gcc	tct	atc	ttg	ctc	atg	aca	gtc	ata	812
148	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	Met	Thr	Val	Ile	
149					185					190					195		
151	agc	att	gac	cgg	ttt	ctg	gct	gtg	gtg	tat	ccc	atg	cag	tcc	ctc	tcc	860
152	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met	Gln	Ser	Leu	Ser	
153				200					205				210				
155	tgg	cgt	act	ctg	gga	agg	gct	tcc	ttc	act	tgt	ctg	gcc	atc	tgg	gct	908
156	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu	Ala	Ile	Trp	Ala	
157			215					220					225				
159	ttg	gcc	atc	gca	ggg	gta	gtg	cct	ctc	gtc	ctc	aag	gag	caa	acc	atc	956
160	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys	Glu	Gln	Thr	Ile	
161	230					235					240						
163	cag	gtg	ccc	ggg	ctc	aac	atc	act	acc	tgt	cat	gat	gtg	ctc	aat	gaa	1004
164	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	Val	Leu	Asn	Glu	
165	245				250					255					260		
167	acc	ctg	ctc	gaa	ggc	tac	tat	gcc	tac	tac	ttc	tca	gcc	ttc	tct	gct	1052
168	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser	Ala	Phe	Ser	Ala	
169				265					270						275		
171	gtc	ttc	ttt	ttt	gtg	cgc	ctg	atc	att	tcc	acg	gtc	tgt	tat	gtg	tct	1100
172	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val	Cys	Tyr	Val	Ser	
173				280				285					290				
175	atc	att	cga	tgt	ctt	agc	tct	tcc	gca	gtt	gcc	aac	cgc	agc	aag	aag	1148
176	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn	Arg	Ser	Lys	Lys	
177			295				300					305					
179	tcc	cgg	gct	ttg	ttc	ctg	tca	gct	gct	gtt	ttc	tgc	atc	ttc	atc	att	1196
180	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys	Ile	Phe	Ile	Ile	
181	310					315				320							
183	tgc	ttc	gga	ccc	aca	aac	gtc	ctc	ctg	att	gcg	cat	tac	tca	ttc	ctt	1244
184	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His	Tyr	Ser	Phe	Leu	
185	325				330					335					340		
187	tct	cac	act	tcc	acc	aca	gag	gct	gcc	tac	ttt	gcc	tac	ctc	ctc	tgt	1292
188	Ser	His	Thr	Ser	Thr	Glu	Ala	Ala	Tyr	Phe	Ala	Tyr	Leu	Leu	Cys		
189				345					350					355			
191	gtc	tgt	gtc	agc	agc	ata	agc	tgc	tgc	atc	gac	ccc	cta	att	tac	tat	1340
192	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro	Leu	Ile	Tyr	Tyr	
193				360				365				370					
195	tac	gct	tcc	tct	gag	tgc	cag	agg	tac	gtc	tac	agt	atc	tta	tgc	tgc	1388
196	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser	Ile	Leu	Cys	Cys	
197			375				380				385						
199	aaa	gaa	agt	tcc	gat	ccc	agc	agt	tat	aac	agc	agt	ggg	cag	ttg	atg	1436
200	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser	Gly	Gln	Leu	Met	
201	390					395					400						
203	gca	agt	aaa	atg	gat	acc	tgc	tct	agt	aac	ctg	aat	aac	agc	ata	tac	1484
204	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn	Asn	Ser	Ile	Tyr	
205	405				410					415				420			
207	aaa	aag	ctg	tta	act	tag	gaaaagggac	tgctgggagg	ttaaaaagaa								1532
208	Lys	Lys	Leu	Leu	Thr												

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209          425
211 aagtttataa aagtgaataa cctgaggatt ctattagtc ccacccaaac tttattgatt 1592
213 cacctcctaa aacaacagat gtacgacttg catacctgct ttttatggga gctgtcaagc 1652
215 atgtattttt gtcaattacc agaaagataa caggacgaga tgacggtggt attccaaggg 1712
217 aatattgcc aatgctacagt aataaatgaa tgtcacttct ggatatagct aggtgacata 1772
219 tacatactta catgtgtgta tatgtagatg tatgcacaca catatattat ttgcagtgca 1832
221 gtatagaata ggcactttta aacactcttt ccccgacccc cagcaattat gaaaataatc 1892
223 tctgattccc tgattttaata tgcaaagtct aggttggttag agtttagccc tgaacatttc 1952
225 atgggtgttca tcaacagtga gagactccat agtttgggct tgtaccactt ttgcaaataa 2012
227 gtgtattttg aaattgtttg acggcaaggt ttaagttatt aagaggtaag acttagtact 2072
229 atctgtgcgt agaagttcta gtgttttcaa ttttaaacat atccaagttt gaattcctaa 2132
231 aattatggaa acagatgaaa agcctctggt ttgatatggg tagtattttt tacattttac 2192
233 aactgtaca cataagccaa aactgagcat aagtcctcta gtgaatgtag gctggctttc 2252
235 agagtaggct attcctgaga gctgcatgtg tccgcccccg atggaggact ccaggcagca 2312
237 gacacatgcc agggccatgt cagacacaga ttggccagaa accttctctg tgagcctcac 2372
239 agcagtgaga ctggggccac tacatttgct ccactctctt gggattggct gtgaactgat 2432
241 catgtttatg agaaactggc aaagcagaat gtgatctctt agggagtaat gaccatgaaa 2492
243 gacttctcta cccatcttaa aaacaacgaa agaaggcatg gacttctgga tgcccatcca 2552
245 ctgggtgtaa acacactctag tagttgttct gaaatgtcag ttctgatatg gaagcaccca 2612
247 ttatgcgctg tggccactcc aatagggtct gagtgtacag agtggaataa gacagagacc 2672
249 tgccctcaag agcaaagtag atcatgcata gagtgtgatg tatgtgtaat aaatatgttt 2732
251 cacacaaaca aggcctgtca gctaaagaag tttgaacatt tgggttacta tttcttggg 2792
253 ttataactta atgaaaacaa tgcagtacag gacatatatt ttttaaaata agtctgattt 2852
255 aattgggcac tatttattta caaatgtttt gctcaataga ttgctcaaat cagggtttct 2912
257 tttagaatc aatcatgtca gtctgcttag aaataacaga agaaaataga attgacattg 2972
259 aaatctagga aaattattct ataatttcca tttacttaag acttaatgag actttaaaag 3032
261 ctttttttaa cctcctaagt atcaagtata gaaaatcttc atggaattca caaagtaatt 3092
263 tggaaattag gttgaaacat atctcttctt ttacgaaaaa atggtagcat tttaaacaaa 3152
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267 ctgtaatccc agcacttttg gaggtgagg cgggtggatc acgaggtcag gagatcgaga 3272
269 ccactctggc taacacggtg aaaccgctct ctactaaaaa tgcaaaaaaa attagccggg 3332
271 cgtggtggca ggcacctgta gtcccagcta ctggggaggc tgaggcagga gactggcgtg 3392
273 aacccaggag gcgaccttg tagtgagccg agatcgcgcc actgtgctcc agcctgggca 3452
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281 <213> ORGANISM: Homo sapiens
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293 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
294          35          40          45
297 Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
298          50          55          60
301 Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
302 65          70          75          80

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305 Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu
306      85      90      95
309 Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val
310      100      105      110
313 Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile
314      115      120      125
317 Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu
318      130      135      140
321 Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser
322 145      150      155      160
325 Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg
326      165      170      175
329 Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu
330      180      185      190
333 Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met
334      195      200      205
337 Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu
338      210      215      220
341 Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys
342 225      230      235      240
345 Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp
346      245      250      255
349 Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser
350      260      265      270
353 Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile Ile Ser Thr Val
354      275      280      285
357 Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn
358      290      295      300
361 Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys
362 305      310      315      320
365 Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His
366      325      330      335
369 Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala
370      340      345      350
373 Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro
374      355      360      365
377 Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
378      370      375      380
381 Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
382 385      390      395      400
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390      420      425
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394 <211> LENGTH: 548
395 <212> TYPE: DNA
396 <213> ORGANISM: Homo sapiens
398 <400> SEQUENCE: 7

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VERIFICATION SUMMARY

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